

**AMENDMENTS TO THE CLAIMS:**

This listing of claims will replace all prior versions,  
and listings of claims in the application:

**LISTING OF CLAIMS:**

**1-43. (canceled)**

**44. (withdrawn)** Mutated V1/AR1/AV1 or C1/AL1/AC1 gene sequence of a tomato infecting geminivirus wherein the mutations consist of point mutations distributed along the sequence in such a way that the continuous homology between the mutated sequence and the corresponding viral gene sequence is below or equal to 8 nucleotides, preferably below or equal to 5 nucleotides, said mutated sequence encoding for a capsid protein or for a Rep protein, respectively.

**45. (withdrawn)** Mutated V1/AR1/AV1 gene sequence according to claim 44, encoding for a capsid protein having sequence SEQ ID No 7.

**46. (withdrawn)** Mutated C1/AL1/AC1 gene sequence according to claim 44, wherein the mutation further comprises a truncation occurring at 3' terminal so that the mutated sequence encodes for a truncated Rep protein.

**47. (withdrawn)** Mutated C1/AL1 /AC1 gene sequences according to claim 46, wherein the truncated Rep proteins consist of 130 aminoacids (Rep 130) to 210 aminoacids (Rep 210).

**48. (withdrawn)** Mutated C1/AL1/AC1 gene sequence according to claim 46 encoding for Rep 210 SEQ ID No 3 or SEQ ID No 5.

**49. (withdrawn)** Mutated C1/AL1/AC1 gene sequence encoding for Rep 130 SEQ ID No 9.

**50. (withdrawn)** Mutated gene sequence according to claim 44 wherein the tomato infecting geminivirus is TYLCSV.

**51. (withdrawn)** Synthetic construct comprising an heterologous polynucleotide sequence containing in the 5'-3' direction:

- a) polynucleotide sequence acting as promoter in said plant or tissue or transformed cells;
- b) a non translated polynucleotide sequence positioned 5' of the encoding region;
- c) a mutated gene sequence;
- d) a sequence acting as transcription terminator, positioned 3' with respect to the mutated gene sequence.

**52. (withdrawn)** Expression vector comprising the construct as defined according to claim 51.

**53. (withdrawn)** Transgenic plant, tissue or plant cells thereof, comprising in their genome a mutated gene sequence according to claim 43.

**54. (withdrawn)** Seed comprising in its genome a mutated gene sequence according to claim 43.

**55. (previously presented)** A method for the preparation of transgenic plants, plant tissue or cells thereof having long lasting resistance against geminiviruses, including the following steps:

a) identification or selection of a geminivirus gene-derived sequence encoding an amino acid sequence able to confer resistance against geminiviruses;

b) mutagenesis of the geminivirus gene-derived sequence, wherein the mutations consist of point mutations distributed along the geminivirus gene-derived sequence so that continuous homology between the mutated sequences and the corresponding viral gene sequence is less than or equal to 8 nucleotides or less than or equal to 5 nucleotides;

c) insertion of the geminivirus gene sequence mutated in the step b) in the plant, plant tissue or cell thereof, using a construct comprising an heterologous polynucleotide sequence containing in the 5'-3' direction:

- i) a polynucleotide sequence acting as promoter in said plant or tissue or transformed cells;
- ii) a non translated polynucleotide sequence positioned 5' of the encoding region;
- iii) a polynucleotide sequence encoding a geminivirus-derived amino acid sequence, properly mutagenised according to step (b) to be an ineffective target of the post-transcriptional gene silencing induced by the infecting geminivirus;
- iv) a sequence acting as transcription terminator positioned 3' with respect to said polynucleotide sequence.

**56-57. (cancelled)**

**58. (previously presented)** The method according to claim 55, wherein the geminiviruses are selected from the species belonging to the Begomovirus genus and isolates thereof.

**59. (currently amended)** The method according to claim 58, wherein the Begomoviruses species is TYLCSV Tomato yellow leaf curl Sardinia virus (TYLCSV).

**60. (cancelled)**

**61. (previously presented)** The method according to claim 55, wherein the gene sequence is selected from the group consisting of C1/AL1/AC1 belonging to TYLCSV.

**62. (cancelled)**

**63. (previously presented)** The method according to claim 61, wherein the amino acid sequence is a truncated protein with respect to the viral wild-type protein.

**64. (previously presented)** The method according to claim 63 wherein the viral gene sequences made ineffective targets of the virus-induced posttranscriptional gene silencing is SEQ ID No 8.

**65. (currently amended)** The method according to claim 64, wherein the truncated protein is Rep-130 ~~(SEQ ID No 9)~~ having the sequence of SEQ ID No 9.

**66-67. (cancelled)**

**68. (currently amended)** The method according to claim 55, wherein the plants, tissues or cells thereof belong to a member selected from the group consisting of tomato, pepper, tobacco, squash, manioc, sweet potato, cotton, melon, potato, soybean, corn, wheat, sugar cane, bean, and beet.